



## SEQUENCE LISTING

<110> Duvert-Frances, Valerie  
Pin, Jean-Jacques  
Valladeau, Jenny  
Clair, Valerie  
Saeland, Sem  
Lebecque, Serge J.E.

<120> Antibodies to Mammalian Langerhans Cell Antigen and Their Uses

<130> SF0820K2

<140> US 09/787,192  
<141> 2001-03-15

<150> PCT/US99/22269  
<151> 1999-09-23

<150> EP 99 400 394.5  
<151> 1999-02-18

<150> EP 98 402 374.7  
<151> 1998-09-25

<160> 12

<170> PatentIn version 3.2

<210> 1  
<211> 1547  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (56)..(1039)

<400> 1  
ctggaaaggg cagccagaag cacctgtgct cccaggataa gggtagcac tcagg atg 58  
Met  
1

act gtg gag aag gag gcc cct gat gcg cac ttc act gtg gac aaa cag 106  
Thr Val Glu Lys Glu Ala Pro Asp Ala His Phe Thr Val Asp Lys Gln  
5 10 15

aac atc tcc ctc tgg ccc cga gag cct cct ccc aag tcc ggt cca tct 154  
Asn Ile Ser Leu Trp Pro Arg Glu Pro Pro Pro Lys Ser Gly Pro Ser  
20 25 30

ctg gtc ccg ggg aaa aca ccc aca gtc cgt gct gca tta atc tgc ctg 202  
Leu Val Pro Gly Lys Thr Pro Thr Val Arg Ala Ala Leu Ile Cys Leu  
35 40 45

acg ctg gtc ctg gtc gcc tcc gtc ctg ctg cag gcc gtc ctt tat ccc 250  
Thr Leu Val Leu Val Ala Ser Val Leu Leu Gln Ala Val Leu Tyr Pro  
50 55 60 65

cgg ttt atg ggc acc ata tca gat gta aag acc aat gtc cag ttg ctg	298
Arg Phe Met Gly Thr Ile Ser Asp Val Lys Thr Asn Val Gln Leu Leu	
70 75 80	
aaa ggt cgt gtg gac aac atc agc acc ctg gat tct gaa att aaa aag	346
Lys Gly Arg Val Asp Asn Ile Ser Thr Leu Asp Ser Glu Ile Lys Lys	
85 90 95	
aat agt gac ggc atg gag gca gct ggc gtt cag atc cag atg gtg aat	394
Asn Ser Asp Gly Met Glu Ala Ala Gly Val Gln Ile Gln Met Val Asn	
100 105 110	
gag agc ctg ggt tat gtg cgt tct cag ttc ctg aag tta aaa acc agt	442
Glu Ser Leu Gly Tyr Val Arg Ser Gln Phe Leu Lys Leu Lys Thr Ser	
115 120 125	
gtg gag aag gcc aac gca cag atc cag atc tta aca aga agt tgg gaa	490
Val Glu Lys Ala Asn Ala Gln Ile Gln Ile Leu Thr Arg Ser Trp Glu	
130 135 140 145	
gaa gtc agt acc tta aat gcc caa atc cca gag tta aaa agt gat ttg	538
Glu Val Ser Thr Leu Asn Ala Gln Ile Pro Glu Leu Lys Ser Asp Leu	
150 155 160	
gag aaa gcc agt gct tta aat aca aag atc cgg gca ctc cag ggc agc	586
Glu Lys Ala Ser Ala Leu Asn Thr Lys Ile Arg Ala Leu Gln Gly Ser	
165 170 175	
ttg gag aat atg agc aag ttg ctc aaa cga caa aat gat att cta cag	634
Leu Glu Asn Met Ser Lys Leu Leu Lys Arg Gln Asn Asp Ile Leu Gln	
180 185 190	
gtg gtt tct caa ggc tgg aag tac ttc aag ggg aac ttc tat tac ttt	682
Val Val Ser Gln Gly Trp Lys Tyr Phe Lys Gly Asn Phe Tyr Tyr Phe	
195 200 205	
tct ctc att cca aag acc tgg tat agt gcc gag cag ttc tgt gtg tcc	730
Ser Leu Ile Pro Lys Thr Trp Tyr Ser Ala Glu Gln Phe Cys Val Ser	
210 215 220 225	
agg aat tca cac ctg acc tcg gtg acc tca gag agt gag cag gag ttt	778
Arg Asn Ser His Leu Thr Ser Val Thr Ser Glu Ser Glu Gln Glu Phe	
230 235 240	
ctg tat aaa aca gcg ggg gga ctc atc tac tgg att ggc ctg act aaa	826
Leu Tyr Lys Thr Ala Gly Gly Leu Ile Tyr Trp Ile Gly Leu Thr Lys	
245 250 255	
gca ggg atg gaa ggg gac tgg tcc tgg gtg gat gac acg cca ttc aac	874
Ala Gly Met Glu Gly Asp Trp Ser Trp Val Asp Asp Thr Pro Phe Asn	
260 265 270	
aag gtc caa agt gcg agg ttc tgg att cca ggt gag ccc aac aat gct	922
Lys Val Gln Ser Ala Arg Phe Trp Ile Pro Gly Glu Pro Asn Asn Ala	
275 280 285	
ggg aac aat gaa cac tgt ggc aat ata aag gct ccc tca ctt cag gcc	970
Gly Asn Asn Glu His Cys Gly Asn Ile Lys Ala Pro Ser Leu Gln Ala	
290 295 300 305	

tgg aat gat gcc cca tgt gac aaa acg ttt ctt ttc att tgt aag cga 1018  
 Trp Asn Asp Ala Pro Cys Asp Lys Thr Phe Leu Phe Ile Cys Lys Arg  
                   310                  315                  320

ccc tat gtc cca tca gaa ccg tgacaggaca ggctcccaag ctcactcttt 1069  
 Pro Tyr Val Pro Ser Glu Pro  
                   325

gagctccaac gcttggttaaa catgaggaaa tgcctctttc ttccccagac tccaggatga 1129

ctttgcacgt taatttttct tgcttcaaaa ttgtcccaca gtggcattct ggagtcgctc 1189

tgtcttggtt ggaaattctc tgacgtcttg gaggcagctg gaatggaaag gagaattcag 1249

gttaaagtgg gaggggtggg tagagaggat ttagaagtcc caattgccct gctaaggagg 1309

atcaagaccc gtaatccggc acaacaccct ggggttttcc actctttcag agaaacctca 1369

gcttcatcac atcaaagtta ctccagagca accaagcaat tctcctgata ttgtcatcca 1429

gggcttttct tggccaaacc cctagaatt tccatgtctc tgcttagctg tgctggcagc 1489

tagcagctgg ctgtgtttgc agtgcaaata gctctgttct tggaaatcct gctcatgg 1547

<210> 2

<211> 328

<212> PRT

<213> Homo sapiens

<400> 2

Met Thr Val Glu Lys Glu Ala Pro Asp Ala His Phe Thr Val Asp Lys  
 1                  5                  10                  15

Gln Asn Ile Ser Leu Trp Pro Arg Glu Pro Pro Pro Lys Ser Gly Pro  
                   20                  25                  30

Ser Leu Val Pro Gly Lys Thr Pro Thr Val Arg Ala Ala Leu Ile Cys  
                   35                  40                  45

Leu Thr Leu Val Leu Val Ala Ser Val Leu Leu Gln Ala Val Leu Tyr  
                   50                  55                  60

Pro Arg Phe Met Gly Thr Ile Ser Asp Val Lys Thr Asn Val Gln Leu  
 65                  70                  75                  80

Leu Lys Gly Arg Val Asp Asn Ile Ser Thr Leu Asp Ser Glu Ile Lys  
                   85                  90                  95

Lys Asn Ser Asp Gly Met Glu Ala Ala Gly Val Gln Ile Gln Met Val  
                   100                  105                  110

Asn Glu Ser Leu Gly Tyr Val Arg Ser Gln Phe Leu Lys Leu Lys Thr  
 115 120 125

Ser Val Glu Lys Ala Asn Ala Gln Ile Gln Ile Leu Thr Arg Ser Trp  
 130 135 140

Glu Glu Val Ser Thr Leu Asn Ala Gln Ile Pro Glu Leu Lys Ser Asp  
 145 150 155 160

Leu Glu Lys Ala Ser Ala Leu Asn Thr Lys Ile Arg Ala Leu Gln Gly  
 165 170 175

Ser Leu Glu Asn Met Ser Lys Leu Leu Lys Arg Gln Asn Asp Ile Leu  
 180 185 190

Gln Val Val Ser Gln Gly Trp Lys Tyr Phe Lys Gly Asn Phe Tyr Tyr  
 195 200 205

Phe Ser Leu Ile Pro Lys Thr Trp Tyr Ser Ala Glu Gln Phe Cys Val  
 210 215 220

Ser Arg Asn Ser His Leu Thr Ser Val Thr Ser Glu Ser Glu Gln Glu  
 225 230 235 240

Phe Leu Tyr Lys Thr Ala Gly Gly Leu Ile Tyr Trp Ile Gly Leu Thr  
 245 250 255

Lys Ala Gly Met Glu Gly Asp Trp Ser Trp Val Asp Asp Thr Pro Phe  
 260 265 270

Asn Lys Val Gln Ser Ala Arg Phe Trp Ile Pro Gly Glu Pro Asn Asn  
 275 280 285

Ala Gly Asn Asn Glu His Cys Gly Asn Ile Lys Ala Pro Ser Leu Gln  
 290 295 300

Ala Trp Asn Asp Ala Pro Cys Asp Lys Thr Phe Leu Phe Ile Cys Lys  
 305 310 315 320

Arg Pro Tyr Val Pro Ser Glu Pro  
 325

<210> 3  
 <211> 10663  
 <212> DNA  
 <213> Homo sapiens

<400> 3

tccctgtccc cactccgcaa tttggtgttc actctacttt cctccatgac ttgactgagg	60
gacttgggtg actcctccct ggagatgact cttggcactg ctggagcatt tcatacaacc	120
caggtctctg ttccagtctt gttgattaaa cccatgggtc tcctccaagc ataaggctgg	180
gccaacccat agtctcaacc agagaaaggg aaaaagtgc caagctgttt tcttcctcca	240
tccttatcca gagaaaatat tagaacccca ggaacacagg aagaggagaa actaaaaaaaa	300
tgagcacaga cttcccgttc tcatcacagc ggtgattttt ttggtcacta ggtctggcca	360
gagttcctct tctgttttga agagcagggc attgtctgag tgcccgggag aactgcccac	420
cttcctgact ggaaagtgtg gccaaaggc ctgcctgctt ctctgtcttt tctcctgcca	480
ggccaggtgc cagatagagc atccagaggt ttgcacagga gaggtgctca ggaaagacct	540
gtagatgagc atgataatag gaagatggct tctgactccc tccctctcca caaagtggga	600
aatgaaactt cctatggttt gggactttta catccacctc ctctgaaacc ccagaaggcc	660
cacagcccac ggattccatg ccttttgctc agcttcctca tgctggaaca gcctttcgcc	720
tagcggtagc tattctacct acctcagcct gcatttccat cacttgaggt aaatgctccc	780
tgctccagcc ccttcctatg ccatgggcca gccgctaagg cttcctcatc ctttcctggg	840
accaatgaga gggcatctgg ggggctctat aaagtataac tcataccaca aaccagcaga	900
gaaaacccaa cttcctgacc gagcggaaat ggacaagaca cttcccaggc acactgtgtg	960
gcggcttctt tcccgcaa at gcctcaggag gagacatgga cccctgcaag gcccttcta	1020
ccagggtctt gagtaatttg gattcttctc tatcccagg cccagaaata ggacaggcta	1080
tgatgaagg gccaggagcc aggagcagaa gggcagagat gattctggag ttaggctggg	1140
tccaagcat gagagtccag aagtggaaca ttctaactc gtctaagccc tgatggaacc	1200
aaggctctgc aaccacacga gccacctgaa gagagtagga atcttcatgg acaccagag	1260
gcaggcagt atgtggagcc aggcctcat attcgggact atcaaagtgt aaaatttaga	1320
gcagacagca ggctggaag ttacagacag gctgggtagg gaagcgatgg gacagaacaa	1380
atgagacacc atctttgcta cccagtttcc ttcccagagc ttcccagtgt ggggtcctct	1440
ctgggttccc tcatccagtc cgagaagcca ctccagcctg agggccggtt agctggagag	1500
agagcatcaa gggcctgtaa ctacaatgag ctgcacatag gcatgggctg agcgtgcagc	1560
cactatcctc ccaagtacca aagggtggcag tagcccctga aagcataggt agatatttcc	1620
ttggccctgt taacttaacc tctaactctg gtccctgata caggctgtca tccagctcca	1680
ctggctcagc ctcagcaggc ccaggacagc tttcttttcc tgcggccaga gcttttgttc	1740

attcctgggt	aaggagtaaa	tcacacttcc	ccttatgctt	ttgcattgaa	gatgaatgag	1800
aacttctgga	gacagtggaa	aaaagcagca	gcttctagaa	ggcagatccc	aggccccaga	1860
ctgtgtaaat	gtctgagtgg	catgatcagc	tatcaagtct	ccaagtcact	taccattcac	1920
acatccatcc	atgcatcctc	tatccatcca	ttcatccatt	cacccatcct	ccaattatct	1980
ggaccaatth	ccttctthth	tcttctcttc	cctccctctt	tcctctcttc	tttctatat	2040
tccaagaaat	atttgtctag	agtctgccat	gtgccaaatt	tctcagattt	ggcagacttc	2100
ttcaaagcat	gagaagccgc	ccaggagaaa	atttagtcct	tcattgagcc	caaatcagct	2160
cttctgtgcc	ctgagcttct	tgcacatatg	gaactctcta	tttaggacta	caaagaagga	2220
gagaggaggt	gcgacagag	agagaggaga	gagaaacaga	acgattccta	gtctgaggtt	2280
gctgagcgcc	cctactthth	ttgaaaatct	cacatgggtgc	aggaagcagg	gaggagaacc	2340
caagtcttag	gtttacactt	tgaatctcca	agttgcatat	tataaaggga	tattgtatca	2400
gccaagatgc	attaataaca	ggaagcagga	tattctattg	caatgggtgc	ctatttggtg	2460
tctctgtctc	caggcttctc	cccaccagtc	tgtctctcac	caggatcaga	gtgatgtttc	2520
tacagtgtcc	ctgtccttgt	ctctctcttg	cctgaagtcc	ttaattggcc	ccatgtcacc	2580
cacaagccag	aggtccagct	ccttgacatg	atcagaagga	tcttcatcat	cagaccccag	2640
gtgcctcttc	aaccccggtg	gcatcccttc	cctggttgaa	tgtatatttt	acattccagc	2700
aatattgcaa	ctattttaca	tttgccaagc	actccatgct	atcttatgct	ccatcctttg	2760
gcatatgctt	atctttctac	tggattthth	tttttcccat	tactccattt	catatgcttc	2820
tttgaactgg	gcatatttgt	ctcttgtgct	catcaccttg	caatttattt	gctcatgtct	2880
gtctttccta	ccagactatg	agctgcttgg	tgcaaggact	gagagttatt	catcactgtg	2940
gccctatgcc	tggtagagca	tcagtacctc	gaaggcactc	agcctgtatt	tgtgggggtg	3000
atggatgggt	ggatggatga	cgagagtctt	acaagagaaa	tgggataggt	ttgggacaag	3060
atggttaatg	tatccatgta	acagaccccc	agagaagaca	acaaatggcc	tcttcttgaa	3120
agctcagact	tctgaggatg	ggagtaagcc	agacaaggta	tctagtcagg	aataggggag	3180
ttgggatgat	atggtgacct	gctgtgggac	tgacttcttg	tttctcttag	ataagagccc	3240
ttggagagac	aggcagccag	aagcacctgt	gctcccagga	taagggtgag	cactcaggat	3300
gactgtggag	aaggaggccc	ctgatgcgca	cttctactgt	gacaaacaga	acatctccct	3360
ctggccccga	gcaagccaca	tcgctgctga	gaacctgctc	cgtgttctgt	gtgcaaacct	3420
gccctttgct	gctccttcaa	cacacattth	cttcttcttc	caacagagcc	tcctcccaag	3480
tccggtccat	ctctggtccc	ggggaaaaca	cccacagtcc	gtgctgcatt	aatctgcctg	3540

acgctgggtcc	tgggtcgccctc	cgctcctgctg	caggccgtcc	tttgtaagtc	ctcatgtttc	3600
atcgtctggg	cttagccct	ctctgtgcc	gccggctccc	ttcagatcga	gaccacttcc	3660
ctgctctccg	ggtttctcct	cctgtggctt	tttcatttgt	ctccttcctc	ctctttccat	3720
gtgcagtaac	aggctgtgct	gccccagta	cggtgagctg	atgctctttc	cctcccaatt	3780
tctgggagat	tattgggatt	agcatttgca	cattggtgct	caaggataca	gtctttgtcc	3840
tcaggaaaca	ttgatctagt	tttacatcct	gtgctatttt	ctccccgtcc	acccccacc	3900
aatctgagct	ctgctccttg	gatctagagc	cttgtggaca	gtccttgaca	gtgcaatgtc	3960
tcctgaccct	gtgaaggacc	gagcctcatg	tatcattggc	cccagctcac	cagatggaga	4020
gcctggccaa	cgagccaaca	gatctccatg	actcagtcctc	ctctccccag	gactcgttgg	4080
tgctgtcttc	attctcctgt	ccctgtgaag	atcacatcta	gggaggcttc	ctgctcattt	4140
gatgttgcat	ggtttatctt	tcttcctttt	ctggctctgt	caggcttcat	ggcctttgct	4200
gctggcagag	ccttcttcct	cctgccaggg	ctccaggaag	cagagcaaag	ggacccaaga	4260
agctgttggg	tttttttttc	tcctctgtg	gcctcgggac	atatttgggc	ttagacttgt	4320
aggctctgag	cagagtcctc	cttgccccat	cctagacccc	tggcctctaa	catcgcatth	4380
tcctcagggc	tcgcctttga	gcctcttgg	ttatctttga	tcctctctct	ggtacccagg	4440
cctgggacct	gagcagaatg	tgaaagtggg	tggggcaagg	gaaggggaga	aacagttht	4500
taatctctc	ttccatgttc	tctggagaag	ccacttccag	attagtggct	ggttcttccc	4560
atggtcacag	aggggccccat	ggacagatgt	gggggagtg	tgctgtccta	gcagatggcc	4620
actgcagggg	tttctgaaaa	cagagggatg	gcaaccaagg	ggtgggggtct	agggggaatc	4680
aagttctggg	gacagtgggtg	gggtctcatg	agggcaccct	ttatcaaagt	ttccctgaac	4740
actcagaaaa	ttcaggaatg	gtttcttaact	cctgcttctg	cttgctgtg	aaatcttttc	4800
acagagagcc	tgtgttttat	caatctcccc	attatctgta	tccacctgtg	ttcctggcac	4860
atggtaggtg	cccattgcac	gtttgttgta	cgtaaataaa	tgattggagg	gttgggggtg	4920
cccattggac	tgtcttgggt	ctttgggaag	cttcagccta	ttccttcctc	tcctttgatc	4980
aacctgacaa	cacccccact	cctgtccctg	ggactccctc	cagctgacct	cctgactttc	5040
tcaatcccag	atccccgggt	tatgggcacc	atatcagatg	taaagaccaa	tgtccagttg	5100
ctgaaagggtc	gtgtgggaca	catcagcacc	ctggattctg	aaattaaaaa	gaatagtgc	5160
ggcatggagg	cagctggcgt	tcagatccag	atggtgaatg	agagcctggg	ttatgtgcgt	5220
tctcagttcc	tgaagttaaa	aaccagtgtg	gagaaggcca	acgcacagat	ccagatctta	5280
acaagaagtt	gggaagaagt	cagtacctta	aatgccccaa	tcccagagtt	aaaaagtgat	5340

ttggagaaaag	ccagtgccttt	aaatacaaaag	atccggggcac	tccagggcag	cttgggagaat	5400
atgagcaagt	tgctcaaacg	acaaagtaag	tgactcagaa	aattacattg	aagctgacca	5460
gtggcccatg	ggatcttacc	tgtcccagac	ctgaggccat	tgggctggtg	ggttggggag	5520
gagagtgggg	gcaaaagagg	ggcagccatg	ggctaggaag	ttaaggagag	agggcttgag	5580
gttggggagg	acttaggggc	tgtaggaga	aaagagacca	gggtccagct	agagctccca	5640
cacaaaagtg	cagaatgtaa	aagcattagg	ggatgtccac	cctggcccac	acctagtcac	5700
ttcccatcaa	gttcctttct	agagtccagg	ggctcagcca	cttgtcatgg	ccgatggagg	5760
gttgcttcct	catcatgggg	aagacactct	ttgtccaacc	tcttgcatga	taacctctcc	5820
agtcacagag	actctattag	tctctgtctg	actttcagga	tttgaaagag	tgctcccta	5880
ctcctataca	aggacccaag	gacaccagcg	cacagctcca	tttgctgctg	tctctgagac	5940
ctcattcaag	tgccccacc	aagccagcat	ccaagaaat	caagaatacc	agcggttact	6000
tttacctctt	gttctctaga	tgatattcta	cagggtggtt	ctcaaggctg	gaagtacttc	6060
aaggggaact	tctattactt	ttctctcatt	ccaaagacct	ggtatagtgc	cgagcagttc	6120
tgtgtgtcca	ggaattcaca	cctgacctcg	gtgacctcag	agagtgagca	ggtgagtgtc	6180
gtgcctatgg	gctctgtgaa	gggggcgtat	gagcactggg	ccagggagga	tgggcaagat	6240
tatactgcgt	gaacaaaaat	ccccaaatat	tgatgacctc	atgaagaagg	attggttctc	6300
agtagcatgt	cgaataaggg	ccggcaaggg	ggctgtgctc	actgtggcta	ctcaaggacc	6360
caggccaag	gagtcttcat	cttaatatgt	ctccacaatt	gctggggcag	gaaaggggaa	6420
cttgacatat	tgtgcaaagc	ttctgcccag	atttaacata	cctcattttt	gcttacattt	6480
cactagctta	agttatgtta	attaagttaa	gtaagttagt	cagtactcct	ggattgggag	6540
gatcctggat	tccagtactc	ctggaacagg	gcagagagga	tctactttcc	atgtgcccag	6600
aaaaaaagaa	atatttgtga	acagccttaa	tgattccaca	tgactcaaga	agtctcctgc	6660
ctggtgaggc	agaaattggg	caggcccttt	tcatctggga	ggtgggatag	cagagcaggt	6720
cagagcctgg	gctctggcgt	agttctagag	cctgaacctt	gccatctaac	tagtcctagc	6780
agcttgggtg	gaatacccaa	cttcaactgg	caaacttcac	tggccctcac	ttgatgaaac	6840
atgcatgggt	atggcacctg	cctcagagga	aaggagagaa	tgcatatgga	cgactcagca	6900
cagtgccgta	tgtggattca	gggtcatttt	aattcaggta	ttatcatatg	aaccattctc	6960
ttgcggtccg	tgctctggag	ttcagctgag	gccttcctgt	gcttcagcac	ctgcttcctg	7020
agtggcagaa	aggcttgagt	cctgagcttg	ttagctgcag	agcagggaca	catcataatc	7080
tggaagatga	aatctgggct	ctgggcaagg	gcaggaagaa	gcttgagagg	ccagtttgtg	7140



cagcgcacatct	gtggggtcagg	gctgtcactg	agcgcagggtg	aagaacacccc	agagacagat	7200
gatcaagctc	caagtgtggc	cgcacctctg	cttatcctgt	ctttcctaca	ggagtttctg	7260
tataaaacag	cgggggggact	catctactgg	attggcctga	ctaaagcagg	gatggaaggg	7320
gactggtcct	gggtggatga	cacgccattc	aacaagggtcc	aaagtgtgag	gtaagcccct	7380
ggagccctcc	gtgccagcct	gactttcccc	ggccatggcc	agggcatgaa	gggagtgggg	7440
gcgatgttcc	ccatgagaca	gggtttctga	ttcttccctg	tcttagagtg	acaggaacat	7500
tgcaaccaag	atcgagcaca	accctgtcac	caactggctg	tggacctgag	ccctccacgc	7560
cctctgggggt	ttggcaacaa	ggccttctac	ctggccagct	tcagggatct	tgtcatgagt	7620
ctaggtcttc	acagtgtggg	tttgtgtagg	gacttgaaag	tgggtgggtg	gtttggcctg	7680
gacttggggc	atgtgaaagc	ttagagggtcg	aagtctcacc	agtccccctc	ctctgaggct	7740
tgggtgcaga	catttgctat	gccattccct	aggacaaaag	cttgggttga	gttaactcat	7800
ttcttctactg	gaaataagtt	ctttttgatt	ttccactttg	taaatccatc	tttttccccg	7860
ctcttggtag	gttctggatt	ccagggtgagc	ccaacaatgc	tgggaacaat	gaacactgtg	7920
gcaatataaa	ggctccctca	cttcaggcct	ggaatgatgc	cccatgtgac	aaaacgtttc	7980
ttttcatttg	taagcgaccc	tatgtcccat	cagaaccgtg	acaggacagg	ctcccaagct	8040
cactctttga	gctccaacgc	ttgttaaaca	tgaggaaatg	cctctttctt	ccccagactc	8100
caggatgact	ttgcacgtta	atTTTTcttg	cttcaaaaatt	gtcccacagt	ggcattctgg	8160
agtccgtctg	tcttggtctg	aaattctctg	acgtcttgga	ggcagctgga	atggaaagga	8220
gaattcaggt	taaagtggga	ggggtgggta	gagaggattt	agaagttcca	attgccctgc	8280
taaggaggat	caagaccctg	aatccggcat	aacaccctgg	ggttttccac	tctttcagag	8340
aaacctcagc	ttcatcacat	caaagttact	ccagagcaac	caagcaattc	tcctgatatt	8400
gtcatccagg	gcttttcttg	gccaaaacccc	ctagaatttc	catgtctctg	cttagctgtg	8460
ctggcagcta	gcagctggct	gtgtttgcag	tgcaaatagc	tctgttcttg	gaaatcctgc	8520
tcattggtatg	tccccagtgg	tttcttcatc	cacatcatct	aaagcctgaa	cccgttcttc	8580
tctggttcaa	gtcagtggct	gacacggact	tgtatctcct	tcagagctcg	gctggcaccc	8640
agcctccctt	ctccttccac	tcccttagta	cactggagtg	ccgagccctg	ccttccaccc	8700
agcgtccatc	cagccctctg	cctcacctct	ccggcacctc	ctcctccttc	tgcatttctc	8760
atcttctctg	gtcttgtgca	tgggaagcag	ccttcagtgc	cttcatgaat	tcaccttcca	8820
gcttctcag	aataaaatgc	tgccctgggtc	aaggactcac	tccaagtgca	ctttttcatt	8880
tctggttgtc	caggtgaata	tgtgggaaag	gcagtctcct	ctggtggaca	tgaagttcta	8940

gggtatcctc	aggaaacatc	tggggagtc	aaaataacaa	ggactgggga	agttccagtc	9000
ctggaaatgc	cacaaaatgt	gaccagtact	tatctctagt	ttttattaaa	gtagagcaag	9060
gtctccaatg	tcacgatctt	ggtgatcttt	cttcttggtt	actgcacaat	cttctagtct	9120
atagctcaat	tcccaagaac	aagtctcagc	aggttcccca	ctcttcacag	agaccaggtt	9180
ccacaggcat	cagttccaaa	tcccaagtcc	agtggctgaa	gctggaatcc	aggcagcagc	9240
caccacagag	aggagaggag	ggtggagtg	gcacaggtct	tcattaaggt	cctcaggaaa	9300
agatgcttcc	ttaaataact	gtaaccagca	gtgtgttggt	ctgggtgcaa	atgggtcaca	9360
gctgagggca	caggcttgta	ttgtaagacc	tgaaatacca	cgtgctgctg	tgacatttta	9420
tgctcacag	ggcccaaaag	acctaaccct	gagttccctg	cctctacca	gatatacct	9480
tgccctcgtt	ccccacctgg	ctaatttctt	atcatctgga	ccagctgcat	gccacccagt	9540
tttctactta	atgggtttca	cttctctgcc	agcctgagaa	actattcaaa	caagccaatc	9600
acatcctcct	acaggaatcc	ggggcatctc	atccttttat	tactacaagg	cctgcctccc	9660
acagccctgg	ctggttcact	ctgctcctga	gggtgacccc	atgtggccct	gtgtggctta	9720
tgatatcttt	ccccagtaga	ctgtatttgt	gactagtaaa	ctgctgccag	tctcacctgc	9780
acagtgtcaa	atgtcttggt	ttggccatct	tgtcctattt	agagcagggg	atccctccct	9840
caccaatgga	ggaaatggga	ggtgacaaga	acaaggctgg	tcggggatct	ctggttggtt	9900
ttggcaaaga	gatgagctgg	gaaaatcaga	ccatttctct	gggaaagaat	ttgaaccagg	9960
aaatagcaag	aggatgaggc	tgtaacaaa	aggaagtga	gctggaaggc	actgagttaa	10020
gagaaaggct	ggaggggccc	tcacgtggca	ttggaagaaa	ctagcaatga	gcagaagcta	10080
tgaggcaggg	gaaagacatg	aatacaggcc	tggcatggtg	gctcatgcct	ataatcccag	10140
cactttggga	ggctgaagtg	ggtgggtcac	ctgaggtcag	gagttcgaga	cagcctggcc	10200
aacatgggtg	aaccccatct	ctactaaaaa	tacaaaaatt	agccgggcat	ggtgggtggc	10260
acctgtaatt	ccaactactt	gggagactga	ggcaggagaa	ttgcttgaat	ctgggaggca	10320
gaggttgtag	tgagctgaga	tcccaccact	gcactccagc	ctgggcaaca	gggcaagact	10380
ttgtttcaaa	aaaaaagaag	tgactgcaga	ggattatagt	tggcagagaa	aagagaacgg	10440
ctcagaggag	tcgcaatgga	ggtcccggag	ggcagcctga	agggctccgg	ctgctcccg	10500
tcccagggtc	gcctcagatc	ctcccagccc	ttctgatcct	cctgggtttct	gtgcatgggg	10560
accttacgag	gctgtgctcc	tgaccccaac	cattgctttt	tcttgaaact	gaaagagcct	10620
gagtcagtga	ggatgtgttt	ttatctggag	tctgtgcccc	agc		10663

<211> 120  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 ggcagccaga agcacctgtg ctcccaggat aagggtgagc actcaggatg actgtggaga 60  
 aggaggcccc tgatgcgcac ttcactgtgg acaaacagaa catctccctc tggccccgag 120

<210> 5  
 <211> 117  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 agcctcctcc caagtccggt ccattctctgg tcccggggaa aacacccaca gtccgtgctg 60  
 cattaatctg cctgacgctg gtccctggctg cctccgtcct gctgcaggcc gtcccttt 117

<210> 6  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 atccccggtt tatgggcacc atatcagatg taaagaccaa tgtccagttg ctgaaaggctc 60  
 gtgtggacaa catcagcacc ctggattctg aaattaaaaa gaatagtgcac ggcattggagg 120  
 cagctggcgt tcagatccag atggtgaatg agagcctggg ttatgtgcgt tctcagttcc 180  
 tgaagttaaa aaccagtgtg gagaaggcca acgcacagat ccagatctta acaagaagtt 240  
 gggaagaagt cagtacctta aatgccccaa tcccagagtt aaaaagtgat ttggagaaag 300  
 ccagtgcctt aaatacaaag atccggggcac tccagggcag cttggagaat atgagcaagt 360  
 tgctcaaacg acaaa 375

<210> 7  
 <211> 152  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 atgatattct acaggtgggt tctcaaggct ggaagtactt caaggggaac ttctattact 60  
 tttctctcat tccaaagacc tggatatagt ccgagcagtt ctgtgtgtcc aggaattcac 120  
 acctgacctc ggtgacctca gagagtgagc ag 152

<210> 8  
 <211> 119  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
gagttttctgt ataaaacagc ggggggactc atctactgga ttggcctgac taaagcaggg 60  
atggaagggg actggtcctg ggtggatgac acgccattca acaaggtcca aagtgcgag 119

<210> 9  
<211> 985  
<212> DNA  
<213> Homo sapiens

<400> 9  
gttctggatt ccaggtgagc ccaacaatgc tgggaacaat gaacactgtg gcaatataaa 60  
ggctccctca cttcaggcct ggaatgatgc cccatgtgac aaaacgtttc ttttcatttg 120  
taagcgaccc tatgtcccat cagaaccgtg acaggacagg ctcccaagct cactctttga 180  
gctccaacgc ttgttaaaca tgaggaaatg cctcttttctt ccccagactc caggatgact 240  
ttgcacgtta atttttcttg cttcaaaatt gtcccacagt ggcattctgg agtccgtctg 300  
tcttggttg aaattctctg acgtcttgga ggcagctgga atggaaagga gaattcaggt 360  
taaagtggga ggggtgggta gagaggattt agaagttcca attgccctgc taaggaggat 420  
caagaccctg aatccggcac aacaccctgg ggttttccac tctttcagag aaacctcagc 480  
ttcatcacat caaagttact ccagagcaac caagcaattc tcctgatatt gtcattccagg 540  
gcttttcttg gccaaacccc ctagaatttc catgtctctg cttagctgtg ctggcagcta 600  
gcagctggct gtgtttgcag tgcaaatagc totgttcttg gaaatcctgc tcatgggatg 660  
tccccagtgg tttcttcac caccatcatc aaagcctgaa cccgtttctt tctggttcaa 720  
gtcagtggct gacacggact tgtatctcct tcagagctcg gctggcacc agcctccctt 780  
ctccttcac tcccttagta cactggagtg ccgagccctg ccttcacccc agcgtccatc 840  
cagcccctgt cctcacctct ccggcacctc ctctccttc tgcatttct atcttctctg 900  
gtcttgtgca tgggaagcag ccttcagtgc cttcatgaat tcaccttcca gcttctcag 960  
aataaaatgc tgctgggtc aagga 985

<210> 10  
<211> 1756  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (266) .. (1243)

<400> 10  
ggcctctttg ctctgttggt gtcttcagtt aagatgatta aaatgtctgt gtaccagggg 60

agtagtcagg	tggtctcctc	atcaaagccc	aattcttagt	caaaaggatg	aagctgtggc	120										
ctctgcctgg	ctaatcgtct	aagccaagaa	ctgggaactt	gggcatgaca	aagtggcctg	180										
ctttttgggt	catttcccgt	ttctttctgg	atgaaaaggt	ccttggggag	acggatattc	240										
agcttttctt	aagccagagg	cagag	atg	ttg	gag	gag	gct	ccc	gaa	gcg	cac	292				
			Met	Leu	Glu	Glu	Ala	Pro	Glu	Ala	His					
			1				5									
ttc	aca	gtg	gac	aaa	cag	aac	atc	tct	ctc	tgg	cct	cga	gag	cct	cct	340
Phe	Thr	Val	Asp	Lys	Gln	Asn	Ile	Ser	Leu	Trp	Pro	Arg	Glu	Pro	Pro	
10					15					20					25	
ccc	aag	caa	gat	ctg	tct	cca	gtt	ctg	agg	aaa	cct	ctc	tgt	atc	tgc	388
Pro	Lys	Gln	Asp	Leu	Ser	Pro	Val	Leu	Arg	Lys	Pro	Leu	Cys	Ile	Cys	
				30					35					40		
gtg	gcc	ttc	acc	tgc	ctg	gca	ttg	gtg	ctg	gtc	acc	tcc	att	gtg	ctt	436
Val	Ala	Phe	Thr	Cys	Leu	Ala	Leu	Val	Leu	Val	Thr	Ser	Ile	Val	Leu	
			45					50					55			
cag	gct	gtt	ttc	tat	cct	agg	ttg	atg	ggc	aaa	ata	ttg	gat	gtg	aag	484
Gln	Ala	Val	Phe	Tyr	Pro	Arg	Leu	Met	Gly	Lys	Ile	Leu	Asp	Val	Lys	
		60					65					70				
agt	gat	gcc	cag	atg	ttg	aaa	ggg	cgt	gtg	gac	aac	atc	agc	acc	ctg	532
Ser	Asp	Ala	Gln	Met	Leu	Lys	Gly	Arg	Val	Asp	Asn	Ile	Ser	Thr	Leu	
	75					80					85					
ggg	tct	gat	ctt	aag	act	gaa	aga	ggg	cgt	gtg	gac	gat	gct	gag	gtt	580
Gly	Ser	Asp	Leu	Lys	Thr	Glu	Arg	Gly	Arg	Val	Asp	Asp	Ala	Glu	Val	
90					95					100				105		
cag	atg	cag	ata	gtg	aac	acc	acc	ctc	aag	agg	gtg	cgt	tct	cag	atc	628
Gln	Met	Gln	Ile	Val	Asn	Thr	Thr	Leu	Lys	Arg	Val	Arg	Ser	Gln	Ile	
			110						115					120		
ctg	tct	ttg	gaa	acc	agc	atg	aag	ata	gcc	aat	gat	cag	ctc	ctg	ata	676
Leu	Ser	Leu	Glu	Thr	Ser	Met	Lys	Ile	Ala	Asn	Asp	Gln	Leu	Leu	Ile	
			125					130					135			
tta	aca	atg	agc	tgg	gga	gag	gtt	gac	agt	ctc	agt	gcc	aaa	atc	cca	724
Leu	Thr	Met	Ser	Trp	Gly	Glu	Val	Asp	Ser	Leu	Ser	Ala	Lys	Ile	Pro	
		140					145					150				
gaa	ctg	aaa	aga	gat	ctg	gat	aaa	gcc	agc	gcc	ttg	aac	aca	aag	gtc	772
Glu	Leu	Lys	Arg	Asp	Leu	Asp	Lys	Ala	Ser	Ala	Leu	Asn	Thr	Lys	Val	
	155					160					165					
caa	gga	cta	cag	aac	agc	ttg	gag	aat	gtc	aac	aag	ctg	ctc	aaa	caa	820
Gln	Gly	Leu	Gln	Asn	Ser	Leu	Glu	Asn	Val	Asn	Lys	Leu	Leu	Lys	Gln	
170				175					180					185		
cag	agt	gac	att	ctg	gag	atg	gtg	gct	cga	ggc	tgg	aag	tat	ttc	tcg	868
Gln	Ser	Asp	Ile	Leu	Glu	Met	Val	Ala	Arg	Gly	Trp	Lys	Tyr	Phe	Ser	
			190					195						200		
ggg	aac	ttc	tat	tac	ttt	tca	cgc	acc	cca	aag	acc	tgg	tac	agc	gca	916
Gly	Asn	Phe	Tyr	Tyr	Phe	Ser	Arg	Thr	Pro	Lys	Thr	Trp	Tyr	Ser	Ala	

205	210	215	
gag cag ttc tgt att tct aga aaa gct cac ctg acc tca gtg tcc tca			964
Glu Gln Phe Cys Ile Ser Arg Lys Ala His Leu Thr Ser Val Ser Ser			
220	225	230	
gaa tcg gaa caa aag ttt ctc tac aag gca gca gat gga att cca cac			1012
Glu Ser Glu Gln Lys Phe Leu Tyr Lys Ala Ala Asp Gly Ile Pro His			
235	240	245	
tgg att gga ctt acc aaa gca ggg agc gaa ggg gac tgg tac tgg gtg			1060
Trp Ile Gly Leu Thr Lys Ala Gly Ser Glu Gly Asp Trp Tyr Trp Val			
250	255	260	
gac cag aca tca ttc aac aag gag caa agt agg agg ttc tgg att cca			1108
Asp Gln Thr Ser Phe Asn Lys Glu Gln Ser Arg Arg Phe Trp Ile Pro			
270	275	280	
ggt gaa ccc aac aac gca ggg aac aac gag cac tgt gcc aat atc agg			1156
Gly Glu Pro Asn Asn Ala Gly Asn Asn Glu His Cys Ala Asn Ile Arg			
285	290	295	
gtg tct gcc ctg aag tgc tgg aac gat ggt ccc tgt gac aat aca ttt			1204
Val Ser Ala Leu Lys Cys Trp Asn Asp Gly Pro Cys Asp Asn Thr Phe			
300	305	310	
ctt ttc atc tgc aag agg ccc tac gtc caa aca act gaa tgacagatct			1253
Leu Phe Ile Cys Lys Arg Pro Tyr Val Gln Thr Thr Glu			
315	320	325	
ggcctgagct cggcatctgt ggggcaacag tgacctggct gaagagatgt ctctctccct			1313
gaggctccaa gattgctctg tacttacgtt tttttcttgc ttgaaaattg tcccaaacac			1373
agcctgtgggt ctttctgtct tggctggcag ttctctgctc ctggaggcct tggaggagct			1433
tgggttaaac ggggtaggac ctgaaaaggg tgtagcagtc cttactgccc aggcgaggca			1493
ggtcagcaca ccaaacaggt tgttttagatt ttctgatcc ttctcagaag ccttggctga			1553
ccatataaaa gctacattca aatatgacca gtatttgagg agacagacat gcccaaattt			1613
aaccatgata caatttatac aacatgtatt agaacacctc atggtatggt caaaatagta			1673
aatatgttgt ttttatgtgc ctattgcaaa taaatgtaaa gacttaaaaa aaaaaaaaaa			1733
aaaaaaaaaa aaaaaaaaaa aaa			1756

<210> 11  
 <211> 326  
 <212> PRT  
 <213> Mus musculus

<400> 11

Met	Leu	Glu	Glu	Ala	Pro	Glu	Ala	His	Phe	Thr	Val	Asp	Lys	Gln	Asn
1				5					10					15	

15

Ile Ser Leu Trp Pro Arg Glu Pro Pro Pro Lys Gln Asp Leu Ser Pro  
20 25 30

Val Leu Arg Lys Pro Leu Cys Ile Cys Val Ala Phe Thr Cys Leu Ala  
35 40 45

Leu Val Leu Val Thr Ser Ile Val Leu Gln Ala Val Phe Tyr Pro Arg  
50 55 60

Leu Met Gly Lys Ile Leu Asp Val Lys Ser Asp Ala Gln Met Leu Lys  
65 70 75 80

Gly Arg Val Asp Asn Ile Ser Thr Leu Gly Ser Asp Leu Lys Thr Glu  
85 90 95

Arg Gly Arg Val Asp Asp Ala Glu Val Gln Met Gln Ile Val Asn Thr  
100 105 110

Thr Leu Lys Arg Val Arg Ser Gln Ile Leu Ser Leu Glu Thr Ser Met  
115 120 125

Lys Ile Ala Asn Asp Gln Leu Leu Ile Leu Thr Met Ser Trp Gly Glu  
130 135 140

Val Asp Ser Leu Ser Ala Lys Ile Pro Glu Leu Lys Arg Asp Leu Asp  
145 150 155 160

Lys Ala Ser Ala Leu Asn Thr Lys Val Gln Gly Leu Gln Asn Ser Leu  
165 170 175

Glu Asn Val Asn Lys Leu Leu Lys Gln Gln Ser Asp Ile Leu Glu Met  
180 185 190

Val Ala Arg Gly Trp Lys Tyr Phe Ser Gly Asn Phe Tyr Tyr Phe Ser  
195 200 205

Arg Thr Pro Lys Thr Trp Tyr Ser Ala Glu Gln Phe Cys Ile Ser Arg  
210 215 220

Lys Ala His Leu Thr Ser Val Ser Ser Glu Ser Glu Gln Lys Phe Leu  
225 230 235 240

Tyr Lys Ala Ala Asp Gly Ile Pro His Trp Ile Gly Leu Thr Lys Ala  
245 250 255

Gly Ser Glu Gly Asp Trp Tyr Trp Val Asp Gln Thr Ser Phe Asn Lys  
 260 265 270

Glu Gln Ser Arg Arg Phe Trp Ile Pro Gly Glu Pro Asn Asn Ala Gly  
 275 280 285

Asn Asn Glu His Cys Ala Asn Ile Arg Val Ser Ala Leu Lys Cys Trp  
 290 295 300

Asn Asp Gly Pro Cys Asp Asn Thr Phe Leu Phe Ile Cys Lys Arg Pro  
 305 310 315 320

Tyr Val Gln Thr Thr Glu  
 325

<210> 12  
 <211> 328  
 <212> PRT  
 <213> Artificial

<220>  
 <223> majority sequence between human and mouse Langerin

<400> 12

Met Leu Val Glu Glu Glu Ala Pro Asp Ala His Phe Thr Val Asp Lys  
 1 5 10 15

Gln Asn Ile Ser Leu Trp Pro Arg Glu Pro Pro Pro Lys Ser Gly Leu  
 20 25 30

Ser Leu Val Leu Gly Lys Thr Leu Thr Val Arg Ala Ala Leu Ile Cys  
 35 40 45

Leu Ala Leu Val Leu Val Ala Ser Val Val Leu Gln Ala Val Leu Tyr  
 50 55 60

Pro Arg Leu Met Gly Thr Ile Leu Asp Val Lys Ser Asp Ala Gln Leu  
 65 70 75 80

Leu Lys Gly Arg Val Asp Asn Ile Ser Thr Leu Gly Ser Asp Leu Lys  
 85 90 95

Thr Glu Ser Gly Gly Val Asp Ala Ala Gly Val Gln Ile Gln Ile Val  
 100 105 110

Asn Thr Ser Leu Gly Arg Val Arg Ser Gln Ile Leu Ser Leu Glu Thr  
 115 120 125



Ser Val Glu Ile Ala Asn Ala Gln Leu Leu Ile Leu Thr Arg Ser Trp  
 130 135 140

Gly Glu Val Ser Ser Leu Ser Ala Gln Ile Pro Glu Leu Lys Ser Asp  
 145 150 155 160

Leu Asp Lys Ala Ser Ala Leu Asn Thr Lys Val Gln Gly Leu Gln Gly  
 165 170 175

Ser Leu Glu Asn Val Ser Lys Leu Leu Lys Gln Gln Ser Asp Ile Leu  
 180 185 190

Glu Val Val Ala Gln Gly Trp Lys Tyr Phe Ser Gly Asn Phe Tyr Tyr  
 195 200 205

Phe Ser Leu Ile Pro Lys Thr Trp Tyr Ser Ala Glu Gln Phe Cys Val  
 210 215 220

Ser Arg Asn Ala His Leu Thr Ser Val Ser Ser Glu Ser Glu Gln Glu  
 225 230 235 240

Phe Leu Tyr Lys Ala Ala Gly Gly Leu Ile His Trp Ile Gly Leu Thr  
 245 250 255

Lys Ala Gly Ser Glu Gly Asp Trp Ser Trp Val Asp Asp Thr Ser Phe  
 260 265 270

Asn Lys Val Gln Ser Ala Arg Phe Trp Ile Pro Gly Glu Pro Asn Asn  
 275 280 285

Ala Gly Asn Asn Glu His Cys Gly Asn Ile Lys Ala Ser Ala Leu Gln  
 290 295 300

Ala Trp Asn Asp Gly Pro Cys Asp Asn Thr Phe Leu Phe Ile Cys Lys  
 305 310 315 320

Arg Pro Tyr Val Gln Ser Thr Glu  
 325